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## Virulence Genes of Escherichia Coli Isolates From Poultry with Colibacillosis

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Avian colibacillosis is responsible for a significant proportion of the mortality in poultry flocks, contributing to extensive economic losses. Avian pathogenic *Escherichia coli*, the causative agent of colibacillosis, possess several putative virulence genes. Their virulence-associated bacterial properties include adherence to the respiratory tract, resistance to the immunological defences, multiplication under iron-restricted conditions, and production of cytotoxic effects. However, the major pathotypes and their role in colibacillosis have not yet been completely elucidated. The objective of this study was to examine colibacillosis isolates for the presence of four major virulence genes previously detected in other countries in Korasan province of Iran. Fifty-two *E. coli* strains were isolated from 52 chickens with clinical signs of colibacillosis, from different poultry farms. Eleven isolates from feces of 11 healthy chickens were used as controls. All isolates were probed by polymerase chain reaction for the presence of the following groups of genes; tsh, cvi, iss, iuc.

Our results showed that the two virulence genes, tsh and iss, were detected significantly more often amongst colibacillosis isolates than in fecal isolates from healthy birds, therefore confirming their pathogenic role in colibacillosis. Association of these two genes were seen in three pathotypes of 12 pathotypes among 52 colibacillosis isolates. None of fecal isolates in healthy chickens had iss gene. It has been suggested that the iss gene is potential target for detection avian pathogenic *Escherichia coli*.

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